

GenCore version 4.5
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Run on: November 20, 1999, 18:00:23 ; Search time 10.28 Seconds

921.194 Million cell updates/sec

Title: US-09-126-945-2
Perfect score: 335

Sequence: 1 MGSASPGGLSSVSPSHLLPP.....GIIRKPDISQRLVYQFVHPI 333

Scoring table: OLIGO

Searched: 77977 seqs, 28268293 residues

Database : SW1SPProt_37:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	7	510	1	ERG_DJONE	P23075 diospylla
2	14	4	114	1	ERG_HUMAN	P41161 homo sapiens
3	14	4	477	1	ERY1_HUMAN	P50549 homo sapiens
4	14	4	477	1	ERY1_MOUSE	P41564 mus musculus
5	14	4	551	1	ERY4_HUMAN	P42688 homo sapiens
6	14	4	551	1	ERY4_MOUSE	P28332 mus musculus
7	10	3	431	1	SAPA_HUMAN	P28334 homo sapiens
8	10	3	431	1	SAPA_MOUSE	P41568 mus musculus
9	10	3	405	1	SABP_HUMAN	P28333 homo sapiens
10	10	3	405	1	DEVB_JMICE	P43700 mycobacteri
11	8	2	447	1	ELK1_MOUSE	P19419 homo sapiens
12	8	2	447	1	ELK1_HUMAN	P41969 mus musculus
13	8	2	447	1	ELK3_MOUSE	P41970 homo sapiens
14	8	2	405	1	ELK3_HUMAN	P41970 mus musculus
15	8	2	548	1	ERG_MOUSE	P51548 mus musculus
16	8	2	478	1	ERG_HUMAN	P70459 mus musculus
17	8	2	478	1	ERG_CHICK	O90887 gallus galli
18	8	2	478	1	ERG_MOUSE	P11308 homo sapiens
19	8	2	473	1	ERG_LYVNA	O01414 lytechinus
20	8	2	272	1	ERG_MOUSE	O01414 mus musculus
21	8	2	24	4	ETG3_DJONE	P28270 mus musculus
22	8	2	64	1	ETG3_MOUSE	P81774 diospylla
23	8	2	102	1	ETG6_DJONE	P23076 diospylla
24	8	2	250	1	ETV3_HUMAN	P41162 homo sapiens
25	8	2	452	1	FLT1_HUMAN	O01543 homo sapiens
26	8	2	452	1	FLT1_MOUSE	P28333 mus musculus
27	8	2	452	1	FLT1_XENLA	P28333 xenopus laevis
28	7	2	431	1	ACDM_MOUSE	P11170 mus musculus
29	7	2	431	1	ACDM_HUMAN	P45952 mus musculus
30	7	2	431	1	ACDM_PIG	P41357 sus scrofa
31	7	2	431	1	ACDM_PIG	P08503 rellus norv
32	7	2	444	1	CEEG_CBPAC	P30508 cephalosporo
33	7	2	686	1	CN21_HUMAN	P28973 homo sapiens
34	7	2	333	1	DCTP_RHOCA	P37735 rhodobacter
35	7	2	270	1	DNA_SEBNA	P47454 strella m
36	7	2	619	1	EGR2_BJARE	O01519 bretyanalis
37	7	2	619	1	ELF1_HUMAN	P30519 homo sapiens
38	7	2	547	1	ELF1_MOUSE	P30519 mus musculus
39	7	2	547	1	ELF1_HUMAN	O01772 mus musculus
40	7	2	610	1	GLIS_TIRPS	O52275 mus musculus
41	7	2	315	1	GAT3_YEAST	O00582 saccharomy
42	7	2	315	1	HAT3_AJRAH	P46502 arabidopsi
43	7	2	311	1	HOM3_BJAFU	P05901 branchiole
44	7	2	311	1	LB4D_HUMAN	O14914 homo sapiens

ALIGNMENTS

44	7	2.1	329	1	LB4D_PIG
45	7	2.1	692	1	YPH5_THIIV

Q29073 sus scrofa
P45365 thlocystis

RESULT	1
ETSA_DROME	
ID	ETSA_DROME
STANDARD;	
PRT;	114 AA
0075.	

DT	01-APR-1993	(REL. 25, CREATED)
DT	01-APR-1993	(REL. 25, LAST SEQUENCE UPDATE)
DT	01-FEB-1995	(REL. 31, LAST ANNOTATION UPDATE)
DE	DNA-BINDING	PROTEIN-D-EFS-4 (FRAGMENT)

ETS98B OR ETS-4.

OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA.

OC DROSOPHILIDAE; DROSOPHILA

[illegible]

RA
CHEN T., BUNTING M., KARIM F.D., THUMMEL C.S.;
Flotation and characterization of fluoro-phenols

RT an ets-related DNA binding domain

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

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DR PIR; S28821; S28821.
 DR PIR; S28821; S28821.
 DR PIR; S28821; S28821.

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DR      PROSITE; PS00345; ETS_DOMAIN_1; 1.
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DR PROSITE; PS50061; ETS_DOMAIN_3; 1.

DR HSSP: 001543; 1FLI.

FT	NON_TER	1	1	REC_COUNT
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	NON	TER
FT	114	114

Query Match	Score	DB	Length
7.28	24	1	114

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 RKNRPAMNYDKLSRSIROYYKKGI 317

Db 71 RKNRPAMNYDKLSRSIRQYYKGI 94

SECRET

ERM_HUMAN	510 AA
CD_ERM_HUMAN	505 AA
STANDARD:	510 AA

AC P41161;
DE 01-FEB-1985 / BY 31 (CREATED)

DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE ETS-RELATED PROTEIN ERM (ETS TRANSLOCATION VARIANT 5).

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

[illegible]

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ERB1 PROTEIN (ETS TRANSLLOCATION VARIANT 1).
 GN ETV1 OR ETSR1 OR ERB1.
 OS MUS MUSCULUS (MOUSE).
 CC EUARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC ROENTATA: SCIROGNATHI: MORIDA: MORINAE: MDS.
 CC TISSUE-EMBRYO.
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94040714.
 RA BROWN T.A., MCKNIGHT S.L.:
 RT "Specificities of protein-protein and protein-DNA interaction of GABP
 alpha and two newly defined ets-related proteins.";
 RL GENES DEV. 6:2502-2512(1992).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS SEQUENCE 5'-CGA(LA)T-3'.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY. MODERATE LEVELS SEEN IN
 CC THE HEART, BRAIN, LUNG, EMBRYO AND LOWER LEVELS SEEN IN SPLEEN,
 CC INTESTINE, TESTIS AND THYMUS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: J10426; G515964; .
 DR PIR: B46396; B46396.
 DR MGI: 99243; ETSR1.
 DR PROSITE: P50045; ETS_DOMAIN_1; 1.
 DR PROSITE: P50045; ETS_DOMAIN_2; 1.
 DR PROSITE: P50045; ETS_DOMAIN_3; 1.
 DR PFM: PFM0178; Ets: 1.
 DR HSP: P14921; 25TW.
 DR TRANSCRIPTION REGULATION: NUCLEAR PROTEIN; DNA-BINDING.
 FM DNA_BIND 335 415
 FT ETS-DOAIN.
 SQ SEQUENCE 477 AA: 55040 MW: 6704077 CRC32:

Query Match 4.2%: Score 14; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 17e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 295 KNRPMNYDKLSRS 308
 Db 379 KNRPMNYDKLSRS 392

RESULT 5
 ETV1_HUMAN STANDARD: PRT: 551 AA.
 AC P43268;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ADENOVIRUS E1A ENHANCER BINDING PROTEIN (E1A-P) (ETS TRANSLLOCATION
 DE VARIANT 1) (FRAGMENT).
 GN ETV1 OR ETSR1 OR ERB1.
 OS HOMO SAPIENS (HUMAN).
 CC EUARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC PRIMATE: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9593380.
 RA FREEDMAN L.S., OSTREMEYER E.A., LYNCH E.D., STABO C.I., MEZA J.E.,
 RA ANDERSON L.M., DOMP P., LEE M.K., ROBBEL S.E., ELLISON J.,
 RA KIM M., KIM M., KIM M., KIM M., KIM M., KIM M., KIM M., KIM M.,
 RA 22 genes from chromosome 17q21: cloning, sequencing, and

RT characterization of mutations in breast cancer families and tumors.";
 RL GENOMICS 25:256-263(1995).
 RN [2]
 RP SEQUENCE OF 90-551 FROM N.A.
 RX MEDLINE: 9181246.
 RA HICSHIN F., TOSHIDA K., FUJINAGA K., KAMIO K., FUJINAGA K.:
 RT "Isolation of a cDNA encoding the adenovirus E1A enhancer binding
 RT protein (E1A-P) from a human cell line.";
 RL NUCLEIC ACIDS RES 21:547-551(1993).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
 CC THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
 CC 5'-(A)G(A)A(T)G-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 DR EMBL: U18018; G602288; .
 DR EMBL: D12765; G219511; .
 DR MIM: 600711; G515964; ETS_DOMAIN_1; 1.
 DR PROSITE: P50045; ETS_DOMAIN_2; 1.
 DR PROSITE: P50045; ETS_DOMAIN_3; 1.
 DR PFM: PFM0178; Ets: 1.
 DR HSP: P14921; 25TW.
 DR TRANSFAC: T00685; .
 FM DNA_BIND 1 1
 FT NUCLEAR-PROTEIN: ACTIVATOR: TRANSCRIPTION REGULATION.
 FM DNA_BIND 1 1
 FT ASP-GLU-RICH (ACIDIC).
 FT DOMAIN 216 312
 FT DNA_BIND 408 488
 FT CONFLICT 91 94
 FT GNS -> EMBL (IN REF. 2).
 SQ SEQUENCE 551 AA: 60570 MW: 14805640 CRC32:

Query Match 4.2%: Score 14; DB 1; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 295 KNRPMNYDKLSRS 308
 Db 452 KNRPMNYDKLSRS 465

RESULT 6
 ETV1_MOUSE STANDARD: PRT: 555 AA.
 AC P28132;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
 DE VARIANT 4).
 GN ETV4 OR PEA3 OR PEA-3.
 OS MUS MUSCULUS (MOUSE).
 CC EUARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC ROENTATA: SCIROGNATHI: MORIDA: MORINAE: MDS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92192459.
 RA XIN J.-H., COMIE A., LACHANCE P., HASSELL J.A.:
 RT "Molecular cloning and characterization of PEA3, a new member of the
 RT ets oncogene family that is differentially expressed in mouse
 RT embryonic cells.";
 RL GENES DEV. 8:181-186(1992).
 CC -1- REGULATORY ROLE DURING EMBRYOGENESIS.

DR PROSITE: PS50061; ETS-DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSP: P14921; 25TW.
 KW DNA-BINDING: NUCLEAR PROTEIN.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 SQ SEQUENCE 430 AA: 46867 MW: 8175095 CRC32:

Query Match 3.0%; Score 10; DB 1; Length 430;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLMGIRN 296
 DB 41 VARLMGIRN 50

RESULT 9
 SAMP_HUMAN STANDARD: PRT: 405 AA.
 AC P28323;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 24, LAST SEQUENCE UPDATE)
 DE PROSITE: BINDING FACTOR ACCESSORY PROTEIN 1B (SAP-1B) (ETS-DOMAIN
 DE PROSITE: SAP-1B)
 GN ELK4 OR SAP1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
 CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92354673.
 RA DARTON S., IRKISMAN R.;
 RT "The structure of the SAP-1, a protein recruited by serum response
 factor to the c-fos serum response element.";
 RL CELL 68:397-612(1992).
 CC -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
 (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
 MAKES EXTENSIVE DNA CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
 CC BIND DNA AUTONOMOUSLY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE, THEY ONLY DIFFER IN THE
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 DR EMBL: M83164; G33035; -;
 DR PIR: A42093; A42093.
 DR MIR: 600246; -;
 DR PROSITE: PS00345; ETS-DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS-DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS-DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSP: P14921; 25TW.
 DR HSP: P14922; 25TW.
 KW DNA-BINDING: NUCLEAR PROTEIN: ALTERNATIVE SPLICING.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 SQ SEQUENCE 405 AA: 44674 MW: 6662136 CRC32:

OY 287 VARLMGIRN 296
 DB 41 VARLMGIRN 50

RESULT 10
 DEVB_MJCLE STANDARD: PRT: 247 AA.
 AC O45700;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DE DEVB PROTEIN HOMOLOG.
 GN DEVB OR B1496-P1.31.
 OS MYCOBACTERIUM LEPRAE.
 OC BACTERIA: FIRMICUTES: ACTINOBACTERIA: ACTINOBACTERIADE:
 CC MYCOBACTERIALES: CONTREXANTINAE: MYCOBACTERIACEAE: MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROBINSON K., SMITH D.R.;
 RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: PUTATIVE OXIDOREDUCTASE.
 CC -1- SIMILARITY: BELONGS TO THE SOL/DEVB FAMILY.
 CC -----
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 CC -----
 DR EMBL: U00013; G469869; -;
 DR PFAM: F01182; Glucosamine_1so; 1.
 RX MEDLINE: 92334979.
 RA JANKNECHT R., NORDHEIM A.;
 RT "Elk-1 protein domains required for direct and SRF-assisted
 SQ SEQUENCE 247 AA: 26160 MW: 2687786 CRC32:

Query Match 2.4%; Score 8; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 MANGVELE 39
 DB 224 MANGVELE 231

RESULT 11
 ID ELK1_HUMAN STANDARD: PRT: 428 AA.
 AC P19419;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-1.
 GN ELK1
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
 CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89203250.
 RA KAO V.N., HUBNER K., ISOBE M., AR-RUSHDI A., CROCE C.M.,
 RA MEDLINE: 92334979.
 RT "Elk-1 protein domains required for direct and SRF-assisted
 RT translocation breakpoints.";
 RL SCIENCE 244:66-70(1989).
 RN [2]
 RP DOMAINS.
 RX MEDLINE: 92334979.
 RA JANKNECHT R., NORDHEIM A.;
 RT "Elk-1 protein domains required for direct and SRF-assisted
 RT DNA-binding.";

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CC NUCLEIC ACIDS RES. 20:3117-3124(1992).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEUS.
CC -1- TISSUE SPECIFICITY: LUNG AND TESTIS.
CC -1- PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
CC AND ERK).
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
CC EMBL: M25269; G318209; -.
CC DR MIM: A11036; T3100K.
CC DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
CC DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
CC DR PROSITE: PS50061; ETS_DOMAIN.3; 1.
CC DR PFAM: PF00178; Ets; 1.
CC DR HSRP: P14921; 25FW.
CC DR TRANSFAC: T00250; -.
CC DR NUCLEAR PROTEIN: DNA-BINDING: PHOSPHORYLATION.
CC FT DNA_BIND 5 133 P->T (IN REF. 2).
CC FT DNA_BIND 5 133 P->T (IN REF. 2).
CC SEQUENCE 428 AA; 44915 MW; 45243DD0 CRC32;

Query Match 2.4%; Score 8; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MWYDKLSR 307
DB 55 MWYDKLSR 62
|||||

RESULT 12
ID ETK1_MOUSE STANDARD: PRT; 429 AA.
AC P41969;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ETK-1.
GN ETK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RN (1)
RA GREGORY D., UNG S., DENHEZ F., DEHEM M., QUATRENNES B., BEGUE A.,
RA STEHELIN D., MARTIN P.;
RA SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RA SEQUENCE OF 5-224 FROM N.A.
RA MEDLINE: 95047310.
RX GIOVANNI A., PINTAS A., MAIRA S.-M., SOBIESZCZUK P., WASLYK B.;
RT "Net: a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A

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CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
CC EMBL: X87257; G31663; -.
CC DR EMBL: Z36939; G35923; -.
CC DR MIM: M610183; ETK1.
CC DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
CC DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
CC DR PROSITE: PS50061; ETS_DOMAIN.3; 1.
CC DR PFAM: PF00178; Ets; 1.
CC DR HSRP: P14921; 25FW.
CC DR NUCLEAR PROTEIN: DNA-BINDING: PHOSPHORYLATION.
CC FT DNA_BIND 5 133 P->T (IN REF. 2).
CC FT DNA_BIND 5 133 P->T (IN REF. 2).
CC SEQUENCE 429 AA; 45243 MW; F78B8069 CRC32;

Query Match 2.4%; Score 8; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MWYDKLSR 307
DB 55 MWYDKLSR 62
|||||

RESULT 13
ID ETK1_HUMAN STANDARD: PRT; 407 AA.
AC P41970;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ETK-3 (ETS-RELATED PROTEIN NET) (SRF ACCESSORY
GN ETK3 OR NET (SAF2).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RN (1)
RA PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
RA SEQUENCE FROM N.A.
RA MEDLINE: 95047310.
RX GIOVANNI A., PINTAS A., MAIRA S.-M., SOBIESZCZUK P., WASLYK B.;
RT "Net: a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
CC ACTIVATE TRANSCRIPTION WHEN COEXRESSED WITH RAS SERUM RESPONSE
CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
CC AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
CC EMBL: J35715; G31523; -.
CC DR MIM: 600247; -.
CC DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
CC DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
CC DR PROSITE: PS50061; ETS_DOMAIN.3; 1.

```


KW PHOSPHORYLATION. 107 ETS-DOMAIN.
 FT DNA_BIND 166 171 POLY-SER.
 FT DOMAIN 166 171 POLY-SER.
 FT DOMAIN 290 293 POLY-SER.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 418 423 POLY-SER.
 FT DOMAIN 456 459 POLY-SER.
 FT MOD_RES 526 526 PHOSPHORYLATION (BY PRK)
 FT MUTAGEN 526 526 T->A: LOSS OF A PHOSPHORYLATION SITE.
 SQ SEQUENCE 548 AA: 58776 MW: 971D76D CRC32:

Query Match Similarity 2.48; Score 8; DB 1; Length 548;
 Percent Identical 100.0%; Pred.No.3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 300 MNYDKLSP 307
 DB 76 MNYDKLSP 83

Search completed: November 20, 1999, 18:05:36
 Job time: 313 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 1999, 18:00:23 : Search time 10.28 seconds
 (without alignments)
 921.194 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 335
 Sequence: 1 MGASAPGSLVSPSHLLLP.....GIIRKPDISORLWGFVHPI 335

Scoring table: OLIGO

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	24	7-2	114	1	ETS4_DROME	P29775 drosophila
2	14	4-2	510	1	ERK_HUMAN	P41161 homo sapien
3	14	4-2	477	1	ETV1_HUMAN	P50549 homo sapien
4	14	4-2	477	1	ETV1_MOUSE	P41164 mus musculu
5	14	4-2	351	1	ETV4_HUMAN	P43266 homo sapien
6	14	4-2	351	1	ETV4_MOUSE	P43266 mus musculu
7	10	3-0	431	1	SAPB_MOUSE	P23323 mus musculu
8	10	3-0	430	1	SAPB_MOUSE	P23323 mus musculu
9	10	3-0	405	1	SAPB_HUMAN	P23323 mus musculu
10	8	2-4	247	1	DEVE_JMCLE	O43700 mycobacteri
11	8	2-4	428	1	ELK1_HUMAN	P14419 homo sapien
12	8	2-4	429	1	ELK1_MOUSE	P41969 mus musculu
13	8	2-4	407	1	ELK3_HUMAN	P41970 homo sapien
14	8	2-4	407	1	ELK3_MOUSE	P41971 mus musculu
15	8	2-4	408	1	ERF_MOUSE	P50548 homo sapien
16	8	2-4	551	1	ERF_MOUSE	P50548 mus musculu
17	8	2-4	478	1	ERG_CHICK	O90837 gallu
18	8	2-4	462	1	ERG_HUMAN	P13308 homo sapien
19	8	2-4	173	1	ERG_LYVIA	O01414 lytechinus
20	8	2-4	272	1	ERK_MOUSE	P81270 mus musculu
21	8	2-4	104	1	ETIS2_DROME	P29774 drosophila
22	8	2-4	104	1	ETIS2_DROME	P29776 drosophila
23	8	2-4	280	1	ETV3_HUMAN	P01543 homo sapien
24	8	2-4	452	1	ETV3_HUMAN	P01543 mus musculu
25	8	2-4	452	1	ETV3_MOUSE	P26333 mus musculu
26	8	2-4	453	1	ETV3_MOUSE	P41157 xenopus lae
27	8	2-4	421	1	ACDM_HUMAN	P11310 homo sapien
28	8	2-4	421	1	ACDM_MOUSE	P45952 mus musculu
29	8	2-4	421	1	ACDM_MOUSE	P41367 sus scrofa
30	8	2-4	421	1	ACDM_MOUSE	P08503 rattus norv
31	8	2-4	444	1	CERG_CYPAC	P08503 rattus norv
32	8	2-4	666	1	CERG_CYPAC	P28973 drosophila
33	8	2-4	270	1	DCTP_RHOCA	P37735 rhodospira
34	8	2-4	333	1	DNA_SERNA	P45454 seretia ma
35	8	2-4	412	1	ESR2_BRARE	O05159 brachydanio
36	8	2-4	619	1	ELF1_HUMAN	P32519 homo sapien
37	8	2-4	619	1	ELF1_MOUSE	O60775 mus musculu
38	8	2-4	157	1	ELF1_MOUSE	O60775 mus musculu
39	8	2-4	157	1	ELF1_MOUSE	O60775 mus musculu
40	8	2-4	610	1	GLMS_THIRP	O51726 methanococ
41	8	2-4	310	1	GRL_YEAST	O00581 saccharomy
42	8	2-4	315	1	HAT3_ARATH	O46602 arabidopsi
43	8	2-4	411	1	HOX3_BRAFL	P50901 brachylocto
44	8	2-4	311	1	LB4D_HUMAN	O14914 homo sapien

44 7 2.1 329 1 LBAD_PIG 029073 sus scrofa
45 7 2.1 692 1 YPH5_THRVI PA5365 thioacytis

ALIGNMENTS

RESULT 1

EST4_DROME STANDARD: PRT: 114 AA.

AC P29775:
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1995 (REL. 25, LAST SEQUENCE UPDATE)
DE DNA-BINDING PROTEIN D-ETS-4 (FRAGMENT).
GN ETS98B OR ETS-4.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
PE PTERODACTYL, ANTHROPOD, TRACHEATA, HEXAPODA, INSECTA,
CC PTEROGOTA, DIPTERA, BRACHYCERA, MISCOMERA, EPHYROIDEA,
CC DROSOPHILINAE, DROSOPHILA.
LN 111
RP SEQUENCE FROM N.A.
RX MEDLINE: 92245640.
RA CHEN T., BUNTING M., KARIM F.D., THUMMEL C.S.:
RT Isolation and characterization of five Drosophila genes that encode
CC the Drosophila DNA-binding domain.
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CC -----
CC EMBL: N88474; G157196; .
DR PIR: S28821; S28821.
DR FLYBASE: FBgn000659; Ets98B.
DR PROSITE: PS00343; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00347; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSP: 001543; 1FEL.
DR DNA-BINDING: NUCLEAR PROTEIN.
FM NON_TER 1
FT DNA_BIND 26 108 ETS-DOMAIN.
FT NON_TER 114 114
SQ SEQUENCE 114 AA: 13051 MW; E9003913 CRC32:

Query Match 7 2%: Score 24; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0y 294 RKNRPANNDKLSRSIRYKKGCI 317
Db 71 RKNRPANNDKLSRSIRYKKGCI 94
|||||

RESULT 2

ERM_HUMAN STANDARD: PRT: 510 AA.

AC P4161:
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ETS-RELATED PROTEIN ERM (ETS TRANSLLOCATION VARIANT 5).
GN ETS OR ERM.
OS HOMO SAPIENS (HUMAN).
PE EUMARTIDA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA:
OC EUMARTIDA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA:

OC PRIMATES: CATARRHINI; HOMININAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-TESTIS.
RA MONTE D., BAERT J.-L., DEFOSSER P.-A., DE LAUNOIT Y., STEHELIN D.:
RT Molecular cloning and characterization of human ERM, a new member of
RT the ETS family closely related to mouse PEA3 and ERK1 transcription
RT factors.
RL ONCOGENE 9:1397-1406(1994).
LN 121
RP SEQUENCE FROM N.A.
RX MEDLINE: 96299763.
RA MONTE D., COUITE L., DEMITTE F., DEFOSSER P.-A., LE CONIAT D.,
RA STEHELIN R., BERGER Y., DE LAUNOIT Y.,
RT GENOMIC ORGANIZATION OF THE HUMAN ERM (ETS5) GENE, A PEA3 GROUP
RT GENE LOCATED AT 3q25.2(1985).
CC FUNCTION: BINDS TO DNA SEQUENCES CONTAINING THE CONSENSUS
CC NUCLEOTIDE CORE SEQUENCE GGAA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
CC EMBL: X6184; G419167; .
DR EMBL: X6184; E225719; JOINED.
DR EMBL: X6182; E225719; JOINED.
DR EMBL: X6183; E225719; JOINED.
DR EMBL: X6187; E225719; JOINED.
DR EMBL: X6177; E225719; JOINED.
DR EMBL: X6176; E225719; JOINED.
DR EMBL: X6175; E225719; JOINED.
DR PIR: S43692; S43692.
DR FLYBASE: FBgn000659; Ets98B.
DR PROSITE: PS00343; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00347; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSP: P14921; 2STW.
DR DNA-BINDING: NUCLEAR PROTEIN.
FM DNA_BIND 368 448
FT NON_TER 510 510
SQ SEQUENCE 510 AA: 57839 MW; 758122BD CRC32:

Query Match 4 2%: Score 14; DB 1; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0y 295 RKNRPANNDKLSRS 308
Db 412 RKNRPANNDKLSRS 425
|||||

RESULT 3

ETVL_HUMAN STANDARD: PRT: 477 AA.

AC P50549:
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS TRANSLLOCATION VARIANT 1 (ERB1 PROTEIN).
GN ETV1 OR ERB1.
OS HOMO SAPIENS (HUMAN).
PE EUMARTIDA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA:
OC EUMARTIDA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA:

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 95215084.
 RA JON I. S., DAVIS J.N., BRAUN B.S., SUBLETT J.E., ROUSSEL M.F.,
 RA DENNY C.T., SHAPIRO D.N.;
 RA The variant Ewing's sarcoma translocation (7;22) fuses the EWS gene to
 RT the breakpoint region of the EWS gene.
 RN ONCOGENE 10:1229-1234(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=KIDNEY;
 RX MEDLINE: 95380185.
 RA MONTE D., COUETTE L., BAERT J.-L., ANGELI I., STEHLEN D.,
 RA MONTAUDO J.;
 RT factor ErbB1.
 CC Molecular cloning and characterization of the ets-related human transcription
 RL factor ErbB1.
 CC ONCOGENE 11:771-779(1995).
 CC [1]
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA[AT]-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -1- TISSUE SPECIFICITY: VERY HIGHLY EXPRESSED IN BRAIN, HIGHLY
 CC INTERESTING PANCREAS AND LUNG AND HEART, MODERATELY IN SPLEEN, SMALL
 CC INTESTINE, PANCREAS AND LUNG, EMBRIO AND LOWER LEVELS SEEN IN SPLEEN,
 CC IN PLACENTA AND PERIPHERAL BLOOD LEUKOCYTES.
 CC -1- DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED BY A
 CC CHROMOSOMAL TRANSLOCATION T(7;22)(p22;q12) WHICH INVOLVES ETV1
 CC AND EWS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: U17163; G596006; -;
 DR EMBL: X87175; G1045061; -;
 DR MIM: 600541; -;
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1;
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1;
 DR PROSITE: PS00347; ETS_DOMAIN_3; 1;
 DR PFM: P00178; Ets; 1;
 DR HSSP: P14921; 2STW.
 DR TRANSSCRIPTION REGULATION; ACTIVATOR; NUCLEAR PROTEIN; DNA-BINDING;
 RM PROTO-ONCOGENE; CHROMOSOMAL TRANSLOCATION.
 CC ETS-DOMAIN.
 FT DNA_BIND 335 415
 FT CONFLICT 39 39 L -> V (IN REF. 2).
 FT CONFLICT 71 79 AQPNDPEFEDVQESL -> V (IN REF. 2).
 FT CONFLICT 117 117 S -> C (IN REF. 2).
 FT CONFLICT 127 127 S -> T (IN REF. 2).
 FT CONFLICT 253 253 MISSING (IN REF. 2).
 FT CONFLICT 349 349 S -> A (IN REF. 2).
 SQ SEQUENCE 477 AA: 55100 MW: 7580133 CRC32:.

Query Match 4.28; Score 14; DB 1; Length 477;
 B. Local Similarity 100.0%; Pred. No. 1; 7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 KMRPANNYDKLSRS 308
 Db 379 KMRPANNYDKLSRS 392

RESULT 4
 ETV1_HUMAN STANDARD; PRT: 477 AA.
 AC P41644
 DT 01-FEB-1995 (REL. 31, CREATED)

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ETV1 PROTEIN (ETS TRANSCRIPTION VARIANT 1).
 OS HOMO SAPIENS OR ETV1.
 OS MUS MUSCULA OR ETV1.
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC ROENTLIA; SCIROGAMPHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=EMBRYO;
 RX MEDLINE: 94040714.
 RA JON I. S., WRIGHT S.L.;
 RA Specific A1; protein and protein-DNA interaction of GABP
 RT alpha and two newly defined ets-related proteins.
 RL GENES DEV. 6:2502-2512(1992).
 CC [1]
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA[AT]-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY, MODERATE LEVELS SEEN IN
 CC INTERESTING PANCREAS AND LUNG, EMBRIO AND LOWER LEVELS SEEN IN SPLEEN,
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: L10426; G51964; -;
 DR EMBL: X6336; B46386;
 DR MIM: 600541; -;
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1;
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1;
 DR PROSITE: PS00347; ETS_DOMAIN_3; 1;
 DR PFM: P00178; Ets; 1;
 DR HSSP: P14921; 2STW.
 DR TRANSSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING.
 RM PROTO-ONCOGENE; CHROMOSOMAL TRANSLOCATION.
 CC ETS-DOMAIN.
 FT DNA_BIND 335 415
 FT CONFLICT 39 39 L -> V (IN REF. 2).
 FT CONFLICT 71 79 AQPNDPEFEDVQESL -> V (IN REF. 2).
 FT CONFLICT 117 117 S -> C (IN REF. 2).
 FT CONFLICT 127 127 S -> T (IN REF. 2).
 FT CONFLICT 253 253 MISSING (IN REF. 2).
 FT CONFLICT 349 349 S -> A (IN REF. 2).
 SQ SEQUENCE 477 AA: 55040 MW: 67040277 CRC32:.

Query Match 4.28; Score 14; DB 1; Length 477;
 B. Local Similarity 100.0%; Pred. No. 1; 7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 KMRPANNYDKLSRS 308
 Db 379 KMRPANNYDKLSRS 392

RESULT 5
 ETV4_HUMAN STANDARD; PRT: 551 AA.
 AC P43366
 DT 01-OCT-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ADEOVIRUS E1A ENHANCER BINDING PROTEIN (E1A-F) (ETS TRANSCRIPTION
 DE VARIANT 4) (FRAGMENT).
 GN ETV4 OR E1AF.
 OS HOMO SAPIENS (HUMAN).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE: 95293180.
 RA FRIEDMAN L.S., OSTERMEYER E.A., LYNCH E.D., SZABO C.I., MEZA J.E.,
 RA ANDERSON L.A., DOMP P., LEE M.K., ROWELL S.E., ELLISON O.,
 RA BOYD J., KING M.C.;
 RT 22 genes from chromosome 17q21: cloning, sequencing, and

RT characterization of mutations in breast cancer families and tumors.*;
 RL GENOMICS 25:256-263(1995).
 RN [2]
 RP MEDLINE: 9318126.
 RX HIGHMANN, R.; TOSHIDA, K.; FUJINAGA, K.; KATO, K.; FUJINAGA, K.;
 RT PROTEIN: A new human member of the ets oncogene family.*;
 RL NUCLEIC ACIDS RES. 21:547-553(1993).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
 CC THE ADOENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
 CC 5'(ACGCGAAT)GT-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC
 DR EMBL: D16018; G302286;
 DR EMBL: D16018; G302286;
 DR MIM: 600713; G219611;
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_3; 1.
 DR PFMW: PF00178; Ets; 1.
 DR HSSP: P14921; 2STW.
 DR TRANSFAC: T00685;
 DR DNA-BINDING: NUCLEAR PROTEIN: ACTIVATOR; TRANSCRIPTION REGULATION.
 RM
 FT DOMAIN 115 142 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 215 311 GLN-RICH
 FT DNA_BIND 408 488 GNGS -> EMSD (IN REF. 2).
 FT CONFLICT 91 94
 SO SEQUENCE 551 AA: 60570 MW: 1180540 CRC32:
 Query Match 4.28; Score 14; DB 1; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2e-06; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 Oy 295 KRPMANNYDKRS 308
 Db 452 KRPMANNYDKRS 465
 RESULT 6
 ID ETV4_MOUSE STANDARD: PRT; 555 AA.
 A 1 555
 RT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
 DE VARIANT 4).
 OS ETV4 OR PEA3 OR PEK-3.
 GN MUS MUSCULUS (MUS).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC EUMETAZOA: SCIROCOGNATHI: MOLLUSCA: MOLLUSCA: MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92192459.
 RA XIN J.-H.; COMIE A.; LACHANCE P.; HASSELL J.A.;
 RT Molecular cloning and characterization of PEA3, a new member of the
 RT Ets oncogene family that is differentially expressed in mouse
 RT embryonic cells. 11:146(1993).
 CC -1- FUNCTION: BINDS TO THE PEA3 MOTIF (5'-AGGAG-3'). MAY PLAY A
 CC REGULATORY ROLE DURING EMBRYOGENESIS.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: EPIDIDYMIS AND THE BRAIN.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC or send an email to license@1sb-slb.ch).
 CC
 DR EMBL: X61230; G302286;
 DR EMBL: X61230; G302286;
 DR MIM: 524923; PEA3.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_3; 1.
 DR PFMW: PF00178; Ets; 1.
 DR HSSP: P14921; 2STW.
 DR TRANSFAC: T00684;
 DR DNA-BINDING: NUCLEAR PROTEIN: ACTIVATOR; TRANSCRIPTION REGULATION;
 RM
 FT PROPHOSPHORYLATED 150 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 217 315 GLN-RICH
 FT DNA_BIND 412 492 ETS-DOMAIN.
 SO SEQUENCE 555 AA: 60846 MW: 1084570E CRC32:
 Query Match 4.28; Score 14; DB 1; Length 555;
 Best Local Similarity 100.0%; Pred. No. 2e-06; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 Oy 295 KRPMANNYDKRS 308
 Db 456 KRPMANNYDKRS 469
 RESULT 7
 ID SAPA_HUMAN STANDARD: PRT; 431 AA.
 A 1 431
 RT 01-FEB-1992 (REL. 24, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
 DE PROTEIN ELK-4).
 OS ELK4 OR SAP1.
 GN HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC EUMETAZOA: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92154673.
 RA DALTON S.; TREISMAN R.;
 RT Characterization of SAP-1, a protein recruited by serum response
 RT factor to the c-fos serum response element.*;
 RL CELL 60:597-612(1992).
 RN [2]
 RP REVISIONS.
 RX MEDLINE: 9412347.
 RX MEDLINE: 9412347.
 RT Characterization of SAP-1, a protein recruited by serum response
 RT factor to the c-fos serum response element.*;
 RL CELL 76:411-411(1994).
 CC -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
 CC (SRF). REQUIRES DNA-BINDING SRF FOR TERNARY COMPLEX FORMATION AND
 CC MAINTAINS EXTENSIVE DNA CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
 CC BIND DNA AUTONOMOUSLY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER IN THE

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CC C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL: M85165; G429186; -.
CC MIM: B42093; B42093.
CC DR PROSITE: P500345; ETS_DOMAIN_1; 1.
CC DR PROSITE: P500346; ETS_DOMAIN_2; 1.
CC DR PROSITE: P500346; ETS_DOMAIN_3; 1.
CC DR PFAM: PF00178; Ets; 1.
CC DR HSPR: P14921; 25TW.
CC DR TRANSFAC: T00737; -.
CC DR DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
CC ETS_DOMAIN_1; 85
CC ETS_DOMAIN_2; 85
CC ETS_DOMAIN_3; 85
CC SEQUENCE 431 AA; 46827 MW; 2560052A CRC32;

Query Match 3.0%; Score 10; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLMGIRKN 296
DB 41 VARLMGIRKN 50

RESULT 8
SAPL_MOUSE STANDARD; PRT; 430 AA.
ID SAPL_MOUSE
RA MEDLINE: 92154673.
RT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SRF-1A) (ETS-DOMAIN
DE ELK4 OR SAP).
GN ELK4 OR SAP.
OS MUS MUSCULUS (MURINE).
OC ROBOTIA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC ROBOTIA: SCIROGOMPHI: MORINAE: MORINAE: MOS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYO.
RA MEDLINE: 95047310.
RA GNEV. A. PINZAS A., MAIRA S.-M., SOBIESZCZUK P., MASLYK B.;
RA "A new ets transcription factor that is activated by Ras."
RA GENES: 815021513(1994).
CC ETS_DOMAIN_1; 85
CC ETS_DOMAIN_2; 85
CC ETS_DOMAIN_3; 85
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: LUNG AND LIVER.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL: M85165; G429186; -.
CC MIM: B42093; B42093.
CC DR PROSITE: P500345; ETS_DOMAIN_1; 1.
CC DR PROSITE: P500346; ETS_DOMAIN_2; 1.
CC DR PROSITE: P500346; ETS_DOMAIN_3; 1.
CC DR PFAM: PF00178; Ets; 1.
CC DR HSPR: P14921; 25TW.
CC DR TRANSFAC: T00737; -.
CC DR DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
CC ETS_DOMAIN_1; 85
CC ETS_DOMAIN_2; 85
CC ETS_DOMAIN_3; 85
CC SEQUENCE 405 AA; 44674 MW; C656C13E CRC32;

Query Match 3.0%; Score 10; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR PROSITE: P550061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSPR: P14921; 25TW.
DR DNA-BINDING: NUCLEAR PROTEIN; ETS-DOMAIN
DR DNA_BIND 5
DR SEQUENCE 430 AA; 46867 MW; B8175C55 CRC32;

Query Match 3.0%; Score 10; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLMGIRKN 296
DB 41 VARLMGIRKN 50

RESULT 9
SAPL_HUMAN STANDARD; PRT; 405 AA.
ID SAPL_HUMAN
RA MEDLINE: 92154673.
RT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1B (SRF-1B) (ETS-DOMAIN
DE ELK4 OR SAP).
GN ELK4 OR SAP.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 92154673.
RA GNEV. A. PINZAS A., MAIRA S.-M., SOBIESZCZUK P., MASLYK B.;
RA "A new ets transcription factor that is activated by Ras."
RA GENES: 815021513(1994).
CC ETS_DOMAIN_1; 85
CC ETS_DOMAIN_2; 85
CC ETS_DOMAIN_3; 85
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: LUNG AND LIVER.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL: M85165; G429186; -.
CC MIM: B42093; B42093.
CC DR PROSITE: P500345; ETS_DOMAIN_1; 1.
CC DR PROSITE: P500346; ETS_DOMAIN_2; 1.
CC DR PROSITE: P500346; ETS_DOMAIN_3; 1.
CC DR PFAM: PF00178; Ets; 1.
CC DR HSPR: P14921; 25TW.
CC DR TRANSFAC: T00737; -.
CC DR DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
CC ETS_DOMAIN_1; 85
CC ETS_DOMAIN_2; 85
CC ETS_DOMAIN_3; 85
CC SEQUENCE 405 AA; 44674 MW; C656C13E CRC32;

Query Match 3.0%; Score 10; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 287 VARLWIRKN 296
    |||||||
DB 41 VARLWIRKN 50

RESULT 10
DEV: MICE
DEV: CYCLE STANDARD: PRT: 247 AA.
AC 049700
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE DEVB PROTEIN HOMOLOG.
GN DEVB OR B1496_F1.31.
OS MYCOBACTERIUM THERAE.
OC ACTINOMYCETES: FIRMICUTES: ACTINOBACTERIA: ACTINOBACTERIAE:
CC ACTINOMYCETES: CORNEOBACTERIAE: MYCOBACTERIAE: MYCOBACTERIUM.
CC SEQUENCE FROM N.A.
RP ROBINSON K., SMITH D. R.;
RA SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: PUTATIVE OXIDOREDUCTASE.
CC -1- SIMILARITY: BELONGS TO THE SOL/DEVB FAMILY.
CC -----
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CC -----
DR EMBL: U00013: G466869;
DR PFAM: PF01182: Glucoseamine_1so. 1.
RM OXIDOREDUCTASE.
SO SEQUENCE 247 AA: 26160 MW: D867895 CRC32:

Query Match 2.4%: Score 8; DB 1: Length 247;
Best Local Similarity 100.0%: Pred. No. 1.5;
Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 AAGAVGLE 39
DB 224 AAGAVGLE 231

RESULT 11
ELK1_HUMAN STANDARD: PRT: 428 AA.
ID ELK1_HUMAN
AC P19419;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ELK-1.
OS ELK1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
CC SEQUENCE FROM N.A.
RP MEDLINE: 89203250.
RA REDDY P. S., DEBEN K., ISOB E. M., AR-RUSUDI A., CHOCE C. M.,
RT "elk, tissue-specific ets-related genes on chromosomes X and 14 near
RT translocation breakpoints.";
RL SCIENCE 244:66-70(1989).
RN [2]
RM DOMAINS: 92334979.
RA JARNICKOT R., NORDHEIM A.;
RM ELK-1, protein domains required for direct and SRF-assisted
RM DNA-binding.;

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RL NUCLEIC ACIDS RES. 20:3317-3324(1992).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: LUNG AND TESTIS.
CC -1- MAP PROPORTIONATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
CC AND ERK).
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: M25569: G538209;
DR PIR: A11364; TVERUK.
DR MIR: 311040;
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; ETS; 1.
DR HSPR: P14921; 250.
DR HSPR: P14921; 250.
RM NUCLEAR PROTEIN. DNA-BINDING; PHOSPHORYLATION.
FT DNA BIND 5 86
SO SEQUENCE 428 AA: 44915 MW: 4E43BDP CRC32:

Query Match 2.4%: Score 8; DB 1: Length 428;
Best Local Similarity 100.0%: Pred. No. 2.5;
Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MYWDLR 307
DB 55 MYWDLR 62

RESULT 12
ELK1_MOUSE STANDARD: PRT: 429 AA.
ID ELK1_MOUSE
AC P41565;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ELK-1.
OS ELK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
CC PRIMATES: SCIROGNATHI: MURIDAE: MURINAE: MUR.
CC SEQUENCE FROM N.A.
RP STEIN-CEBEL: TISSUE-EMBRYO:
RA GREVIN D., UNG S., DENHEZ F., DEHEM M., QUANTENENS B., BEGUE A.,
RA STEHLIN D., MARTIN P.;
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RM SEQUENCE OF 5-224 FROM N.A.
RP MEDLINE: 95007310.
RA GIOVANE A., PINTZAS A., MAYRA S.-M., SOBIESZCZUK P., WASYLK B.;
RT "Nc1, a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A

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CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
CC -1 SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: X87257; G836635; -
DR EMBL: Z36939; G535923; -
DR MGI: MGI:101833; ELK1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PFAM: PF00178; Ets; 1.
DR HSP: P14921; 25TW.
DR NUCLEAR PROTEIN: DNA-BINDING; PHOSPHORYLATION.
KT DNA_BIND 5 86 ETS-DOMAIN.
FT CONFLICT 133 133 P -> T (IN REF. 2).
SQ SEQUENCE 429 AA; 45243 MW; F7BE8069 CRC32.

Query Match 2.4% Score 8; DB 1; Length 429;
Best Local Similarity 100.0%; Freq. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MWYKRLSR 307
DB 55 MWYKRLSR 62
|||||||
RESULT 13
ELK3_HUMAN STANDARD; PRT; 407 AA.
AC P41970.
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (SRF ACCESSORY
DE ELK3 OR NET.
GN ELK3 OR NET.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC [MIMMOTUS; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA GIOVANE A.; PINTZAS A.; MAIRA S.-M.; SOBIESZCZAK P.; WASYLK B.;
RA GLOVANE A.; PINTZAS A.; MAIRA S.-M.; SOBIESZCZAK P.; WASYLK B.;
RE GENES DEV. 8:1502-1513(1994).
RT FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
RT FORM A TRANS-REPRESSION COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
RT AND SRF MOIETIES OF THE FOS/SPERM RESPONSE ELEMENT.
CC -1 SUBCELLULAR LOCATION: NUCLEAR.
CC -1 SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: Z36715; G531523; -
DR MIM: 600247; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00061; ETS_DOMAIN_3; 1.

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DR PFAM: PF00178; Ets; 1.
DR HSP: P14921; 25TW.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
KT DNA_BIND 5 85 ETS-DOMAIN.
FT DNA_BIND 207 212 POLY-ALA.
SQ SEQUENCE 407 AA; 44365 MW; D0FE221D CRC32.

Query Match 2.4% Score 8; DB 1; Length 407;
Best Local Similarity 100.0%; Freq. No. 2.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MWYKRLSR 307
DB 54 MWYKRLSR 61
|||||||
RESULT 14
ELK3_MOUSE STANDARD; PRT; 409 AA.
AC P41971; P97747; 062346;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (ETS-RELATED
DE ELK3 OR NET.
GN ELK3 OR NET OR ERP.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA GIOVANE A.; PINTZAS A.; MAIRA S.-M.; SOBIESZCZAK P.; WASYLK B.;
RA GLOVANE A.; PINTZAS A.; MAIRA S.-M.; SOBIESZCZAK P.; WASYLK B.;
RE GENES DEV. 8:1502-1513(1994).
RT FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
RT FORM A TRANS-REPRESSION COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
RT AND SRF MOIETIES OF THE FOS/SPERM RESPONSE ELEMENT.
CC -1 SUBCELLULAR LOCATION: NUCLEAR.
CC -1 SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: Z32815; G479113; -

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DR EMBL: L19953: G436189: -
 DR EMBL: S82864: G1836130: -
 DR MGD: MGI:101762: ELK3.
 DR PROSITE: PS00345: ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR PROSITE: PS50061: ETS_DOMAIN_3: 1.
 DR PIR: P00128: ELK3.
 DR PIR: P00129: ELK3.
 DR TRANSFAC: T01413: -
 DR TRANSCRIPTION REGULATION: ACTIVATOR: REPRESSOR: NUCLEAR PROTEIN:
 KM DNA-BINDING:
 FT DNA_BIND 5 85 ETS-DOMAIN.
 FT DOMAIN 208 212 POLY-ALA.
 FT CONFLICT 152 152 Q -> E (IN REF. 1).
 FT CONFLICT 158 158 N -> Y (IN REF. 3).
 FT CONFLICT 159 159 N -> Y (IN REF. 3).
 FT CONFLICT 331 331 A -> T (IN REF. 3).
 FT SEQUENCE 409 AA: 44445 MW: 07556166 CRC32.

Query Match 2.4% Score 8: DB 1: Length 409:
 Best Local Similarity 100.0%: Pred. No. 2.4:
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Oy 300 MNYDKSLR 307
 Db 54 MNYDKSLR 61

RESULT 15
 ERF_HUMAN STANDARD: PRT: 548 AA.
 1D ERF_HUMAN 0-303:48: 1995 (REL. 34, CREATED)
 1C 0-303:48: 1995 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1995 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
 DN ERF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RA SEQUENCE FROM N.A.
 RX SCOURAS D.N., ATMANAGIOTIS M.A., BEAL G.J. JR., FISHER R.J., BLAIR D.G.,
 RA MAYORIALAS-SITIS G.J.:
 RT "ERF: an Ets domain protein with strong transcriptional repressor activity, can suppress ets-associated tumorigenesis and is regulated by phosphorylation during cell cycle and mitogenic stimulation.";
 RT EMBL J. 14:4781-4793(1995).
 RL -1- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1 ELEMENT OF THE ETS PROMOTER. MAY REGULATE OTHER GENES INVOLVED IN CELL GROWTH.
 CC ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
 CC -1- SUPERCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
 CC -1- PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 CC EMBL: U15655: G1015337: -
 DR PROSITE: PS00345: ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR PROSITE: PS50061: ETS_DOMAIN_3: 1.
 DR PIR: P00128: ELK3: 1.
 DR PIR: P00129: ELK3: 1.
 DR TRANSCRIPTION REGULATION: REPRESSOR: DNA-BINDING: NUCLEAR PROTEIN:

KM PHOSPHORYLATION.
 FT DNA_BIND 27 107 ETS-DOMAIN.
 FT DOMAIN 166 171 POLY-SER.
 FT DOMAIN 290 293 POLY-GLY.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 448 453 POLY-PRO.
 FT DOMAIN 454 459 POLY-SER.
 FT MOTIFS 526 526 PHOSPHORYLATION (BY ERK2).
 FT MUTAGEN 526 526 T->A: LOSS OF A PHOSPHORYLATION SITE.
 FT SEQUENCE 548 AA: 58776 MW: 97107680 CRC32.

Query Match 2.4% Score 8: DB 1: Length 548:
 Best Local Similarity 100.0%: Pred. No. 3.1:
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Oy 300 MNYDKSLR 307
 Db 76 MNYDKSLR 83

Search completed: November 20, 1999, 18:05:36
 Job time: 313 sec
 GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 1999, 18:00:23 : Search time 10.28 Seconds

Title: US-09-126-945-2
 Perfect score: 335
 Sequence: 1 MGSASPGSLVSPSHLLLP.....GIIRKPDICRLYQFVAPI 335

Scoring table: OLIGO
 Searched: 77977 seqs, 28268293 residues
 Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	24	7.2	114	1	ERS4_DROME	P29775 drosophila
2	14	4.2	510	1	ERM_HUMAN	P41161 homo sapien
3	14	4.2	477	1	ERV1_HUMAN	P50549 homo sapien
4	14	4.2	477	1	ERV1_HUMAN	P11164 mus musculu
5	14	4.2	551	1	ERV1_HUMAN	P43268 homo sapien
6	14	4.2	555	1	ERV1_HUMAN	P28322 mus musculu
7	10	3.0	431	1	SHPL_HUMAN	P28324 homo sapien
8	10	3.0	420	1	SHPL_HUMAN	P28325 mus musculu
9	10	3.0	420	1	SHPL_HUMAN	P28326 mus musculu
10	8	2.4	247	1	DEBR_MYCLE	O49700 mycobacteri
11	8	2.4	428	1	ELK1_HUMAN	P19419 homo sapien
12	8	2.4	429	1	ELK1_HUMAN	P19419 mus musculu
13	8	2.4	407	1	ELK3_HUMAN	P41970 homo sapien
14	8	2.4	409	1	ELK3_HUMAN	P41971 mus musculu
15	8	2.4	548	1	ERF_MOUSE	P50548 mus musculu
16	8	2.4	551	1	ERF_MOUSE	P70439 mus musculu
17	8	2.4	445	1	ERF_MOUSE	P70439 mus musculu
18	8	2.4	445	1	ERF_MOUSE	P70439 mus musculu
19	8	2.4	173	1	ERG_LYTA	O01414 lytechinus

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20      8      2 4      272 1  ERG_MOUSE
21      8      2 4      64 1  ETS3_DROME
22      8      2 4      102 1 ETS6_DROME
23      8      2 4      250 1 ETV3_HUMAN
24      8      2 4      452 1 ETV3_HUMAN
25      8      2 4      452 1 ETV3_HUMAN
26      8      2 4      452 1 ETV3_HUMAN
27      8      2 4      452 1 ETV3_HUMAN
28      7      2 1      421 1 ACDFM_MOUSE
29      7      2 1      421 1 ACDFM_MOUSE
30      7      2 1      421 1 ACDFM_MOUSE
31      7      2 1      441 1 ACDFM_MOUSE
32      7      2 1      686 1 CNG1_HUMAN
33      7      2 1      373 1 DCFP_HUMAN
34      7      2 1      412 1 DCFP_HUMAN
35      7      2 1      412 1 DCFP_HUMAN
36      7      2 1      619 1 ELP1_HUMAN
37      7      2 1      612 1 ELP1_MOUSE
38      7      2 1      157 1 FBI1_METTA
39      7      2 1      610 1 GLMS_TRIPE
40      7      2 1      310 1 GTRI_YEAST
41      7      2 1      415 1 HATY_ASAH
42      7      2 1      415 1 HATY_ASAH
43      7      2 1      311 1 LB4D_HIG
44      7      2 1      329 1 LB4D_HIG
45      7      2 1      692 1 YPH5_THIYI

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ALIGNMENTS

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RESULT 1
ETS4_DROME STANDARD: PRT: 114 AA.
AC P29775;
01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE D-BOUNDING PROTEIN P-ETS-4 (FRAGMENT).
GN ETS98B OR ETS-4
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA: METAZOA: ARTHROPODA: TRACHEATA: HEXAPODA: INSECTA:
OC PTERYGOTA: DIPTERA: BRACHYCERA: MUSCOMORPHA: EPYRIDOIDEA.
OC DROSOPHILINAE: DROSOPHILA.
NM (1)
NM MEDLINE: 9232964.
RA CHEN T, BURNING W, KARIM F D, THINDEL C S.;
RT "Isolation and characterization of five drosophila genes that encode
an ets-related DNA binding domain."
RL DEV. BIOL. 151:176-191(1992).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC
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CC
DR EMBL: X88474; G157196; -
DR FLYBASE: FB1008259; ETS98B
DR PROSITE: PS00345; ETS DOMAIN_1; 1
DR PROSITE: PS00346; ETS DOMAIN_2; 1
DR PROSITE: PS00061; ETS DOMAIN_3; 1
DR PFAM: PF00178; Ets; 1
DR HSP: 001543; 1BL1
DR DNA-BINDING: NUCLEAR PROTEIN.
FM NON_TER 1
FM DNA-BIND 26 108 ETS-DOMAIN.

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ET NON_TER 114 114
SQ SEQUENCE 114 AA; 13051 MW; E9003913 CRC32;

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 114;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 294 RRRPANNNDLRSIRYKKG1 317
DB 71 RRRPANNNDLRSIRYKKG1 94

RESULT 2
ERM_HUMAN STANDARD: PRT: 510 AA.
AC P1151; 1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 36, LAST SEQUENCE UPDATE)
DE ETS-RELATED PROTEIN ERM (ETS TRANSCRIPTION VARIANT 5).
GN ETV5 OR ERM.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
NM (1)
NM MEDLINE: 94203669.
RA MONTE D., BAERT J.-L., DEPOSEZ P.-A., DE LAUNOIT Y., STEHELIN D.;
RT "Molecular cloning and characterization of human ERM, a new member of
the Ets family closely related to mouse PEA3 and ERM1 transcription
factors."
RN 121
RN GENOMICS 35:236-240(1996).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: UNOCTICUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC
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CC
DR EMBL: X76184; G479167; -
DR EMBL: X96381; E255719; JOINED.
DR EMBL: X96380; E255719; JOINED.
DR EMBL: X96376; E255719; JOINED.
DR EMBL: X96378; E255719; JOINED.
DR EMBL: X96377; E255719; JOINED.
DR EMBL: X96376; E255719; JOINED.
DR PIR: S43692; S43692.
DR MM: 601600;
DR PROSITE: PS00345; ETS DOMAIN_1; 1
DR PROSITE: PS00346; ETS DOMAIN_2; 1
DR PROSITE: PS00061; ETS DOMAIN_3; 1
DR PFAM: PF00178; Ets; 1
DR HSP: P14921; 2STW
DR DNA-BINDING: NUCLEAR PROTEIN.

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FT DNA_BIND 368 448 ETS-DOMAIN.
 SQ SEQUENCE 510 AA: 57638 MW: 75812280 CRC32:
 Query Match 4.28: Score 14: DB 1: Length 510:
 Best Local Similarity 100.0%: Pred. No. 1.7e-06:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Y 295 KRPMAMYDKLSRS 308
 DB 412 KRPMAMYDKLSRS 425
 RESULT 3
 ETV1_HUMAN STANDARD: PRT: 477 AA.
 ID ETV1_HUMAN
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ETV1 TRANSLLOCATION VARIANT 1 (ERB1 PROTEIN).
 GN ETV1 OR ERB1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC PRIMATES: CARNIVORIN: HOMINIDAE: HOMO.
 RX SEQUENCE FROM N.A.
 RP MEDLINE: 95215064.
 RA DENN I.-S., DAVIS J.N., BRAUN B.S., SUBLETT J.E., ROUSSEL M.F.,
 RA JEON C.T., SHAPIRO D.N.:
 RT "A variant Ewing's sarcoma translocation (7;22) fuses the EWS gene to
 RT the ETV1 gene ETV1.".
 RL ONCOGENE 10:1229-1234(1995).
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 95180185.
 RX MEDLINE: 95180185.
 RA MONTY D., COUETTE L., BAERT J.-L., ANGELI I., STEHLEIN D.,
 RA DE LAUNOIR Y.:
 RT "Molecular characterization of the ets-related human transcription
 RT factor ERB1.".
 RL ONCOGENE 11:771-779(1995).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA(AT)-3'.
 CC -1- TISSUE SPECIFICITY: VERY HIGHLY EXPRESSED IN BRAIN, HIGHLY
 CC EXPRESSED IN TESTIS, LUNG AND HEART, MODERATELY IN SPLEEN, SMALL
 CC INTESTINE, PANCREAS AND COLON. WEAKLY IN LIVER, PROSTATE AND
 CC THYMUS. VERY WEAKLY IN SKELETAL MUSCLES, KIDNEY AND OVARY AND NOT
 CC IN PLACENTA AND PERIPHERAL BLOOD LEUKOCYTES.
 CC -1- DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED BY A
 CC CHROMOSOMAL TRANSLOCATION T(7;22)(p22;p12) WHICH INVOLVES ETV1
 CC AND EWS. THIS INVOLVEMENT OF THE ETS FAMILY
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY
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 CC EMBL: 017163: G596006: -
 CC EMBL: X87175: G1045061: -
 CC MIM: 600541: -
 CC PROSITE: PS00345: ETS_DOMAIN_1; 1;
 CC PROSITE: PS00346: ETS_DOMAIN_2; 1;
 CC PROSITE: PS50061: ETS_DOMAIN_3; 1;
 CC HSPR: P14921: 25TV: 1;
 CC TRANSCRIPTION REGULATION: ACTIVATOR: NUCLEAR PROTEIN: DNA-BINDING:
 CC PROTO-ONCOGENE: CHROMOSOMAL TRANSLOCATION.

FT DNA_BIND 335 415 ETS-DOMAIN.
 FT CONFLICT 39 39 L->V (IN REF. 2).
 FT CONFLICT 61 79 AOVPPNDQEPVDFQWESL -> V (IN REF. 2).
 FT CONFLICT 117 117 S -> C (IN REF. 2).
 FT CONFLICT 117 117 N -> K (IN REF. 2).
 FT CONFLICT 123 123 MISSING (IN REF. 2).
 FT CONFLICT 349 349 MISSING (IN REF. 2).
 SQ SEQUENCE 477 AA: 55100 MW: 75807133 CRC32:
 Query Match 4.28: Score 14: DB 1: Length 477:
 Best Local Similarity 100.0%: Pred. No. 1.7e-06:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Y 295 KRPMAMYDKLSRS 308
 DB 379 KRPMAMYDKLSRS 392
 RESULT 4
 ETV1_MOUSE STANDARD: PRT: 477 AA.
 ID ETV1_MOUSE
 AC P41164:
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ERB1 PROTEIN ETV1 TRANSLLOCATION VARIANT 1).
 GN ETV1 OR ETRSP1 OR ERB1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC ROENTIIA: SCIROGAMNTHI: MURIDAE: MURINAE: MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRO.
 RX MEDLINE: 94040714.
 RA "Specificities of protein-protein and protein-DNA interaction of GABP
 RT alpha and two newly defined ets-related proteins.".
 RL GENES DEV. 6:2502-2512(1992).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA(AT)-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY. MODERATE LEVELS SEEN IN
 CC THE HEART, BRAIN, LUNG, EMBRIO AND LOWER LEVELS SEEN IN SPLEEN.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY
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 CC or send an email to: license@sib-sib.ch).
 CC EMBL: L10426: G515964: -
 CC PIR: B46396: B46396.
 CC MGI: 99254: ETRSP1.
 CC PROSITE: PS00345: ETS_DOMAIN_1; 1;
 CC PROSITE: PS00346: ETS_DOMAIN_2; 1;
 CC PROSITE: PS50061: ETS_DOMAIN_3; 1;
 CC HSPR: P14921: 25TV: 1;
 CC TRANSCRIPTION REGULATION: NUCLEAR PROTEIN: DNA-BINDING:
 CC FT DNA_BIND 335 415 ETS-DOMAIN.
 SQ SEQUENCE 477 AA: 55040 MW: 670AC77 CRC32:
 Query Match 4.28: Score 14: DB 1: Length 477:
 Best Local Similarity 100.0%: Pred. No. 1.7e-06:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Y 295 KRPMAMYDKLSRS 308

Db 379 KNRPMANTRYLSRS 392

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RESULT 5
ID ETV4_HUMAN STANDARD: PRT: 551 AA.
AC P43268;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE ADENOVIRUS E1A ENHANCER BINDING PROTEIN (E1A-F) (ETS TRANSLLOCATION
FRAGMENT 4) (FRAGMENT).
OS E1A ENHANCER BINDING PROTEIN (HUMAN)
OS HOMO SAPIENS (HUMAN)
OC EURARCTOTA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: HOMINIDE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95293380.
RX FRIEDMAN L.S., OSTREMEYER E.A., LYNCH E.D., SZABO C.I., MEZA J.E.,
RX BOYD K.W., DOMP P., LEE M.K., ROWELL S.E., ELLISON J.,
RT "22 genes from chromosome 17q21, cloning, sequencing, and
RT characterization of mutations in breast cancer families and tumors."
RL GENOMICS 25:256-263(1995).
RN [2]
RP SEQUENCE OF 90-551 FROM N.A.
RX MEDLINE: 93181245.
RX HIGASHINO F., YOSHIDA K., FUJINAGA K., KAMITO K., FUJINAGA K.;
RT "The E1A protein of adenovirus encoding the adenovirus E1A enhancer binding
RT protein: a new human protein and the E1A oncogene family."
RL NUCLEIC ACIDS RES 21:547-553(1993).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
CC THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
CC 5'-[AGCGGATAT]GT-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
DR EMBL: U01018; G603288;
DR EMBL: D12765; G319611;
DR MIM: 600711;
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR HSP: PF00178; ETS; 1.
DR HSP: PF00178; ETS; 1.
DR TRANSFAC: T00685;
DR DNA-BINDING: NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION.
KW NON-TER 1
FT DOMAIN 116 142 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 215 311 GLN-RICH.
FT DNA_BIND 408 488 ETS-DOMAIN.
FT CONFLICT 91 94 GNGS -> EMD (IN REF. 2).
SQ SEQUENCE 551 AA; 60570 MW; 118D5E60 CRC32;

```

Query Match 4.2%; Score 14; DB 1; Length 551;

Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

295 KNRPMANTRYLSRS 308
452 KNRPMANTRYLSRS 465

```

RESULT 6
ID ETV4_MOUSE STANDARD: PRT: 555 AA.
AC P28322;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE ADENOVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
FRAGMENT 4) (FRAGMENT).
OS E1A ENHANCER BINDING PROTEIN (HUMAN)
OS HOMO SAPIENS (HUMAN)
OC EURARCTOTA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: HOMINIDE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92192459.
RX FRIEDMAN L.S., OSTREMEYER E.A., LYNCH E.D., SZABO C.I., MEZA J.E.,
RX BOYD K.W., DOMP P., LEE M.K., ROWELL S.E., ELLISON J.,
RT "22 genes from chromosome 17q21, cloning, sequencing, and
RT characterization of mutations in breast cancer families and tumors."
RL GENES DEV. 6:481-496(1992).
CC -1- FUNCTION: BINDS TO THE PEA3 MOTIF (5'-AGCAAG-3'). MAY PLAY A
CC REGULATORY ROLE DURING EMBRYOGENESIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: EPIDIDYMIS AND THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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DR EMBL: X63190; G53628;
DR PIR: S24061;
DR MGD: M6199423; PEA3.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR HSP: PF00178; ETS; 1.
DR HSP: PF00178; ETS; 1.
DR TRANSFAC: T00684;
DR DNA-BINDING: NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION.
KW NON-TER 1
FT DOMAIN 124 150 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 212 315 GLN-RICH.
FT DNA_BIND 412 498 ETS-DOMAIN.
SQ SEQUENCE 555 AA; 60846 MW; 084F57CE CRC32;

```

Query Match 4.2%; Score 14; DB 1; Length 555;

Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

295 KNRPMANTRYLSRS 308
456 KNRPMANTRYLSRS 469

Query Match 4.2%; Score 14; DB 1; Length 551;

Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

295 KNRPMANTRYLSRS 308
452 KNRPMANTRYLSRS 465

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CC -----
CC PLS: M52369; G358035; -
CC PLS: A9053; A42092.
CC DR MIM: 600246; -
CC DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
CC DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
CC DR PROSITE: PS0061; ETS_DOMAIN_3; 1.
CC DR PFM: P40178; ETS; 1.
CC DR HSP: P4921; 25FW.
CC DR DNA-BIND: T02128.
CC FT DNA-BIND: 5 NUCLEAR. ETS-DOMAIN.
CC FT DNA-BIND: 85 ETS-DOMAIN.
CC SQ SEQUENCE 405 AA: 44674 MW: C6EC15E CRC32.

Query Match 3.0%; Score 10; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLMGIRN 296
DB 41 VARLMGIRN 50

RESULT 10
DEVB.MYCLE STANDARD; PRT: 247 AA.
AC 049700:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE DEVB PROTEIN HOMOLOG.
OS MCHACTRIN.1.1.1.
OS MCHACTRIN.1.1.1.
OC BACTERIA: FIRMICUTES: ACTINOBACTERIA: ACTINOBACTERIA:
OC ACTINOMYCETALES: CORNBACTERIAE: MYCOBACTERIAE: MYCOBACTERIUM.
FN [1]
RP SEQUENCE FROM N.A.
RA ROBISON K., SMITH D.R.;
LC SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC - SIMILARITY: BELONGS TO THE SOL/DEVB FAMILY.
CC -----
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CC -----
CC EMBL: U00013; G466869; -
CC DR PFM: P01182; Glucosamine_1so; 1.
CC DR OXIDOREDUCTASE.
CC KW
CC SQ SEQUENCE 247 AA: 26160 MW: D8671BF6 CRC32:

Query Match 2.4%; Score 8; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 AAGAVGLE 39
DB 224 AAGAVGLE 231

RESULT 11
ELK1.HUMAN

ID ELK1.HUMAN STANDARD; PRT: 428 AA.
AC P1919; 1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ELK-1.
GN ELK1.
OS HOMO SAPIENS (HUMAN).
OC ERYTHROCYTES; METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA;
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
CC PLS: A9053; A42092.
CC DR MIM: 600246; -
CC DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
CC DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
CC DR PROSITE: PS0061; ETS_DOMAIN_3; 1.
CC DR PFM: P40178; ETS; 1.
CC DR HSP: P4921; 25FW.
CC DR DNA-BIND: T02128.
CC FT DNA-BIND: 5 NUCLEAR. ETS-DOMAIN.
CC FT DNA-BIND: 85 ETS-DOMAIN.
CC SQ SEQUENCE 428 AA: 44915 MW: 4E43BDFD CRC32:

Query Match 2.4%; Score 8; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MNTDKLSR 307
DB 55 MNTDKLSR 62

RESULT 12
ELK1.HUMAN STANDARD; PRT: 429 AA.
AC P1919; 1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

RP SEQUENCE FROM N.A.
 RX MEDLINE: 97047916.
 RA NOZAKI M., ONISHI Y., KANNO N., ONO Y., FUJIMURA Y.;
 RT Molecular cloning of Elk-3, a new member of the Ets family expressed
 RT during mouse embryogenesis and analysis of its transcriptional
 RT DNP:CELL BIO15:555:962(1996).
 RL DNP:CELL BIO15:555:962(1996).
 CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
 CC ACTIVATE TRANSCRIPTION WHEN COEXRESSED WITH BAF, SRC OR MOS
 CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
 CC AND SER MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEUS.
 CC -1- TISSUE SPECIFICITY: HEART, LIVER, LUNG, KIDNEY AND MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC CC
 CC EMBL: Z23215; G479113; -;
 CC EMBL: L19953; G46185; -;
 CC EMBL: L19953; G46185; -;
 CC MGI: 101762; ELK3.
 DR MGI: 101762; ELK3.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00347; ETS_DOMAIN_3; 1.
 DR HSP: 000422; JANC.
 DR TRANSFAC: T01413; -;
 KW TRANSCRIPTION REGULATION; ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 KM DNA-BINDING.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 FT DOMAIN 208 212 POLY-ALA.
 FT CONFLICT 132 132 Q -> E (IN REF. 1).
 FT CONFLICT 139 139 M -> V (IN REF. 3).
 FT CONFLICT 138 138 A -> T (IN REF. 1).
 FT CONFLICT 331 331 A -> T (IN REF. 1).
 SO SEQUENCE 409 AA; 44445 MW; 0F565166 CRC32;.

Query Match 2.4%; Score 8; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MMYDKLSR 307
 DB 54 MMYDKLSR 61

RESULT 15
 ERF_HUMAN
 ID ERF_HUMAN STANDARD; PRT: 548 AA.
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
 GN ERF.
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PLIATHES; CATARRHINI; HOMINIDAE; HOMO.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96030784.
 RA SCOURAS D.N., ATHANASIOU M.A., BEAL G.J. JR., FISHER R.J., BLAIR D.G.,
 RT ERF: an ETS domain protein with strong transcriptional repressor
 RT activity, can suppress ets-associated tumorigenesis and is regulated
 RT by phosphorylation during cell cycle and mitogenic stimulation.*

RL ERF0 144:781-4793(1995).
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE HI
 CC ELEMENT OF THE ETS PROMOTER. MAY REGULATE OTHER GENES INVOLVED
 CC IN CELLULAR PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: NUCLEUS.
 CC -1- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
 CC PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC CC
 CC EMBL: U15555; G101537; -;
 CC PROSITE: PS00345; ETS_DOMAIN_1; 1.
 CC PROSITE: PS00346; ETS_DOMAIN_2; 1.
 CC PROSITE: PS00347; ETS_DOMAIN_3; 1.
 CC PFM: PF00178; Ets; 1.
 DR HSP: 001543; IELI.
 DR TRANSFAC: T01413; -;
 KW TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; NUCLEAR PROTEIN;
 KM DNA-BINDING.
 FT DNA_BIND 167 177 ETS-DOMAIN.
 FT DOMAIN 290 293 POLY-GLY.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 418 423 POLY-PRO.
 FT DOMAIN 496 499 POLY-GLY.
 FT MOD_RES 526 526 PHOSPHORYLATION (BY ERK2).
 FT MOD_RES 526 526 T->A; LOSS OF A PHOSPHORYLATION SITE.
 SO SEQUENCE 548 AA; 58776 MW; 971D7FD CRC32;

Query Match 2.4%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MMYDKLSR 307
 DB 76 MMYDKLSR 83

Search completed: November 20, 1999, 18:05:36
 Job time: 313 sec